human = SEQ ID NO:12; yeast = SEQ ID NO:14) Comparison of MetAP2 Homologues (mouse = SEQ ID NO:13; rat = SEQ ID NO:17;

mou rat hum yea	mou rat hum yea	mou rat hum yea	ye h r	A T T B	פאמצ
mouse rat human yeast	mouse rat human yeast	mouse rat human yeast	mouse rat human yeast	mouse rat human yeast	mouse rat human yeast
451 YPPLC YPPLC YPPLC YPPLN	361 RMEEG RMEEG RMEEG KMEEG	271 AFTVI AFTVI AFTVI AFTVI	181 KYVMS KYVMS KYVMS RAIKI	91 DADG DGDG DGDG ESKKI	
DIKGS DIKGS DIKGS	EVYA EVYA EVYA EHFA:	FUPK	SWIKE SWIKE SWIKE	ATGKF AAGKF ATGKF	EQAA: EEAS: EEVAJ
451 YPPLCDIKGSYTAQF YPPLCDIKGSYTAQF YPPLCDIKGSYTAQF YPPLNDIPGSYTAQF	361 RMEEGEVYAIETFGS RMEEGEVYAIETFGS RMEEGEVYAIETFGS RMEEGEVYAIETFGS	271 AFTVTFNPKYDILLT AFTVTFNPKYDILLK AFTVTFNPKYDTLLK AFTVFNPKYDTLLK AFTVSFDPQYDNLLA	195 KYVMSWIKPGMTMIE KYVMSWIKPGMTMIE KYVMSWIKPGMTMIE KYVMSWIKPGMTMIE	91 105 DADGATGKKKKKKKK DGDGAAGKKKKKKKK DGDGATGKKKKKKKKK ESKKKKNKKKKKKKKK	1 15 MAGVEQAASFGGHLN MAGVEEASSFGGHLN MAGVEEVAASGSHLN
466 EHTILLRPTCKEVVS EHTILCAQPVKKLSA EHTILLRPTCKEVVS EHTILLRPTKEVVS	376 TGKGVVHDDMECSHY TGKGVVHDDMECSHY TGKGVVHDDMECSHY TGKGVVHDDMECSHY TGRGYVTAGGEVSHY	300 AVKDATNTGIKCAGI AVKDATNTGIKCAGI AVKDATNTGIKCAGI AVKDATNTGIKCAGI AVKDATYTGIKEAGI	196 ICEKLEDCSRKLIKE ICEKLEDCSRKLIKE ICEKLEDCSRKLIKE ICEKLEDCSRKLIKE IADMIENTTRKYTGA	PKV PRV PKV	16 GDLDPDDREEGTSST RDLDPDDREEGTSST GDLDPDDREEGAAST
TCKEY	DMEC DMEC DMEC	GIKC GIKC GIKC	CSRKL CSRKL CSRKL	120 QTDPPSVPI QTDPPSVPI QTDPPSVPI	REEG! REEG!
·				_	
RGDDY EEMTIKT RGDDY KGDDY	391 MKNFDI MKNFDI MKNFDI ARSAEI	301 DVRLC DVRLC DVRLC DVRLC	211 NGLNAG NGLNAG NGLNAG ENLLAMED	121 CDLYE CDLYE CDLYE ELLFE	31 AEEA! AEEA! AEEA!
1191	MAČHC AAHD/ AAHD/ AAHD/	DVGEA DVGEA DVGEA	G G	NGVE NGVE NGVE NGVE	KKKKR KKKKR
478 480 478 421	405 MKNFDVGHVPIRLPR MKNFDVGHVPIRLPR MKNFDVGHVPIRLPR MKNFDVGHVPIRLPR ARSAEDHQVMPTLDS	301 DVRLCDVGEAIQEVM DVRLCDVGEAIQEVM DVRLCDVGEAIQEVM DVRLCDVGEAIQEVM DVRLTDIGEAIQEVM	211 225 NGLNAGLA NGLNAGLA NGLNAGLA NGLNAGLA ENLLAMEDPKSQGIG	121 135 CDLYPNGVFPKGQEC CDLYPNGVFPKGQEC CDLYPNGVFPKGQEC CDLYPNGVFPKGQEC	45 AEEAAKKKRRKKKKG AEEAAKKKRRKKKKKG AEEAAKKKRRKKKKKS
	406 TKHL TKHL TKHL AKNL				
	406 TKHLLNVINENFGTL TKHLLNVINENFGTL TKHLLNVINENFGTL TKHLLNVINENFGTL AKNLLKTIDRNFGTL	316 ESYEVEIDGKTYQVK ESYEVEIDGKTYQVK ESYEVEIDGKTYQVK ESYEVEINGETYQVK	226 FPTGCSLNNCAAHYT FPTGCSLNNCAAHYT FPTGCSLNNCAAHYT FPTGCSLNNCAAHYT FPTGLSLNHCAAHFT	136 EYPPTQDGRTAAWRT EYPPTQDGRTAAWRT EYPPTQDGRTAAWRT EYPPTQDGRTAAWRT EYPPTQDGRTAAWRT DYHQDFNLQRTTDEE	46 KGAVSAVQQELDKES KGAVSAGQQELDKES KGPSAAGEQEPDKES
	4 VENEG VENEG VENEG VENEG	SKTYQ SKTYQ SKTYQ SETYQ	2 NCAAH NCAAH NCAAH HCAAH	RTAAI RTAAI RTAAI RTAAI QRTTI	60 SAVQQELDKES SAGQQELDKES AAGEQEPDKES
	421 AFCRRWLD AFCRRWLD AFCRRWLD: PFCRRYLD:	331 PIRNLNGH PIRNLNGH PIRNLNGH PCRNLCGH	241 PNAGDTTV PNAGDTTV PNAGDTTV PNAGDKTV	151 TSEEKKAL TSEEKKAL TSEEKKAL SRYLKRDL	61 GALVD GTSVD GASVD SPASD
	LDRL(LDRL(LDRL(LDRL(GHSI GHSI GHSI	TVLQ TVLQ TVLQ	KALDÇ KALDÇ KALDÇ	EVAKÇ EVAKÇ EVARÇ
	435 RLGESKY RLGESKY RLGESKY RLGQEKY	345 SIGPYRI SIGPYRI SIGQYRI SIAPYRI	241 PNAGDTTVLQYDDIC PNAGDTTVLQYDDIC PNAGDTTVLQYDDIC PNAGDKTVLQYDDIC PNAGDKTVLKYEDVM	165 DQASEEI DQASEEI DQASEEI PQASEEI	61 GALVDEVAKQLESQA GTSVDEVAKQLERQA GASVDEVARQLERSA SPASDLKELNLENEG
	436 LMAI LMAI LMAI LMAI LFAI				
	436 LMALKNLCDLGIVDP LMALKNLCDLGIVDP LMALKNLCDLGIVDP LMALKNLCDLGIVDP	346 HAGKTVPIVKGGEAT HAGKTVPIVKGGEAT HAGKTVPIVKGGEAT HGGKSVPIVKNGDTT	256 KIDFGTHISGRIIDC KIDFGTHISGRIIDC KIDFGTHISGRIIDC KIDFGTHISGRIIDC KVDYGVQVNGNIIDS	166 WNDFREAAEAHRQVR WNDFREAAEAHRQVR WNDFREAAEAHRQVR WNDVRKGAEIHRRVR	76 LEEKERDDDDEDGDG LEEKEKDDDDEDGDG LEDKERDEDDEDGDG VEQQDQAKADESDPV
	DLGIV DLGIV DLGIV RHGLV	VKGGI VKGGI VKGGI VKNGI	SGRI SGRI SGRI	AEAHR AEAHR AEAHR	DDDEI DDDEI EDDEI KADES
	450 VDP VDP VDP	360 EAT EAT EAT	270 IDC IDC IDC	180 QVR QVR QVR QVR	Addi Sabo Sabo Sabo Ode
	443 443 443 386	353 353 353 296	263 263 263 206	180 180 180 116	90 90 90

Dominant Negative Variants fo Mehtionine Aminopeptidase

Inventor(s): Appln. No. Docket #

Chang et al. 09/943,123 66153/45004

Title: Dominant Negative Variants fo Mehtionine Aminopeptidase

Aminopeptidase
Inventor(s): Chang et al.
Appln. No. 09/943,123
Docket # 66153/45004

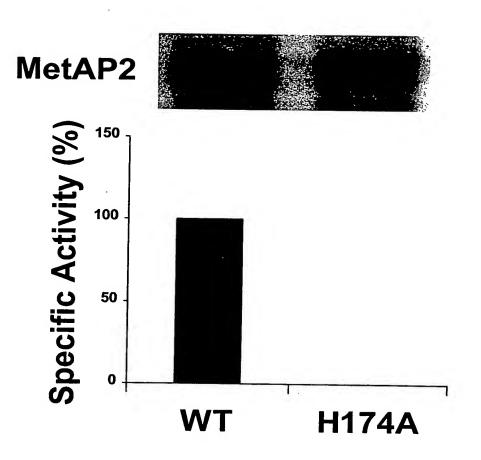
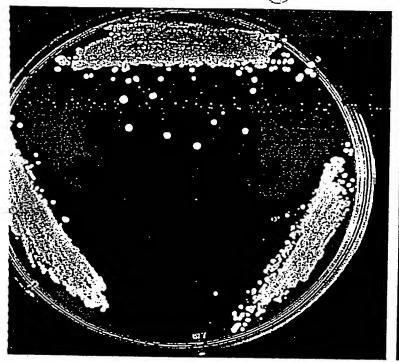
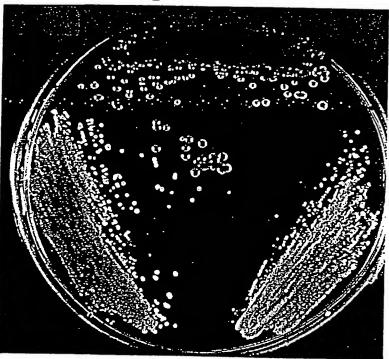


Figure 2





A. Glucose

B. Galactose

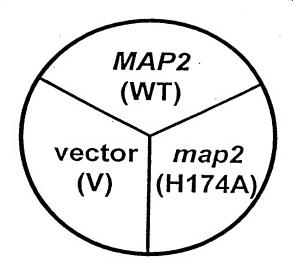


FIGURE 3

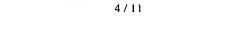
Dominant Negative Variants fo Mehtionine

Inventor(s):

Aminopeptidase Chang et al.

Appln. No. Docket # 09/943,123 66153/45004

Title: Dominant Negative Variants fo Mehtionine Aminopeptidase
Inventor(s): Chang et al.
Appln. No. 09/943,123
Docket # 66153/45004



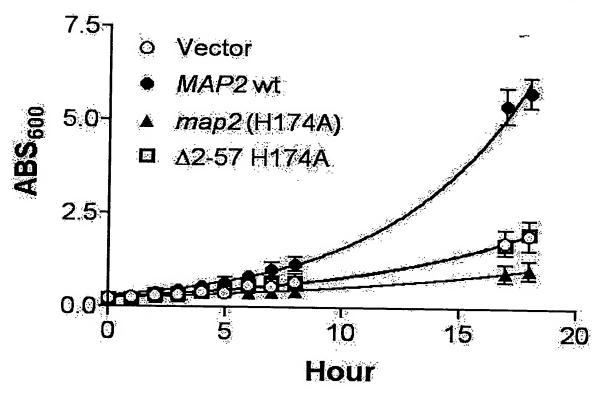
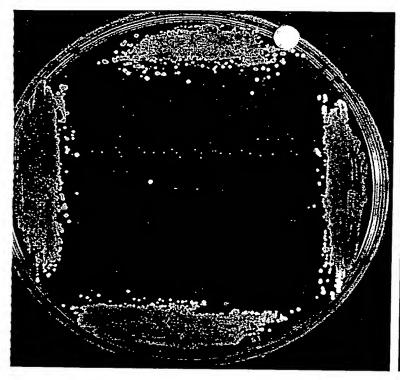
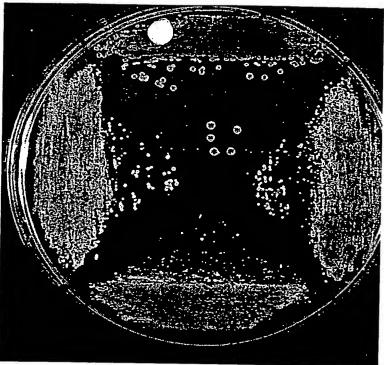


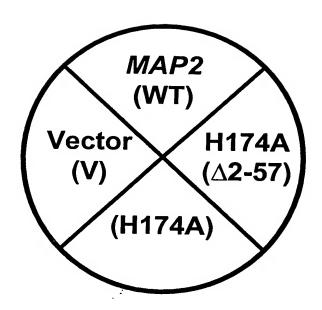
Figure 4





A. Glucose

B. Galactose



H174A-MetAP2 requires N-terminal residues 2-57 for inhibition of map1 Δ growth under the GAL1 promoter.

Figure 5

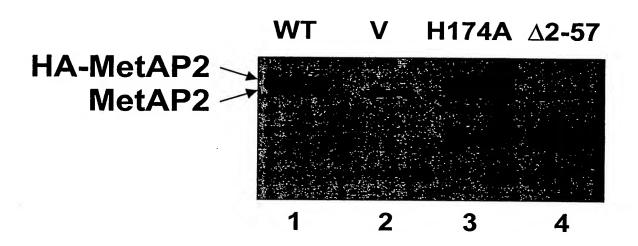
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Dominant Negative Variants fo Mehtionine

Aminopeptidase

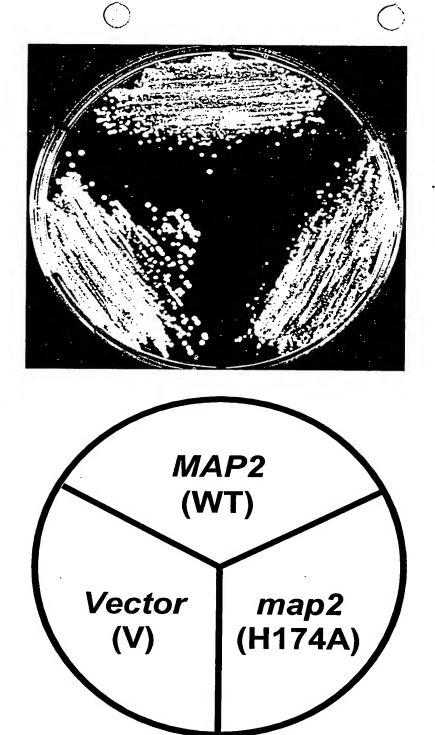
Inventor(s): Appln. No. Docket # Chang et al. 09/943,123 66153/45004

Title: Dominant Negative Variants fo Mehtionine
Aminopeptidase
Inventor(s): Chang et al.
Appln. No. 09/943,123
Docket # 66153/45004



The steady state levels of each MetAP2 construct are comparable. Immunoblot comparison of HA-MetAP2 wt, HA-MetAP2 H174A, and MetAP2 $\Delta 2$ -57 H174A steady state levels in map1 Δ .

Figure 6



Overexpression of H174A-MetAP2 under the GPD promoter does not inhibit the growth of map 2Δ

Figure 7

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Title: Dominant Negative Variants fo Mehtionine

Aminopeptidase Inventor(s):

Chang et al. 09/943,123 Appln. No. 66153/45004 Docket#

Dominant Negative Variants fo Mehtionine

Aminopeptidase

Inventor(s): Appln. No. Docket # Chang et al. 09/943,123 66153/45004

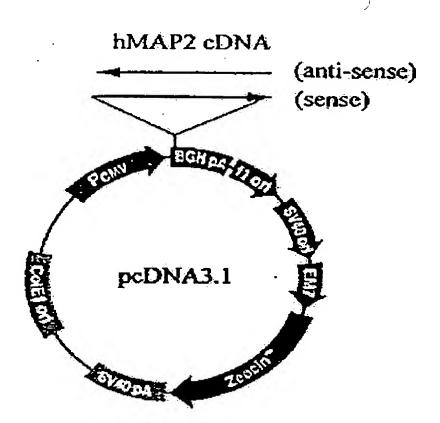


Figure 8

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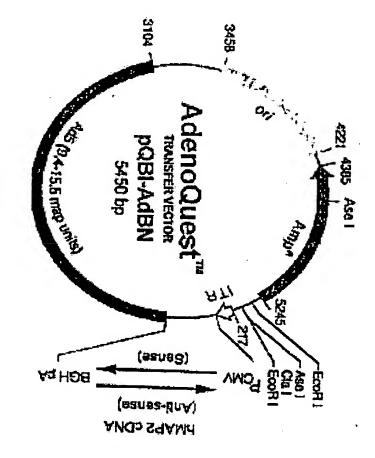


Figure 9

Dominant Negative Variants fo Mehtionine Aminopeptidase

Inventor(s):

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10/11



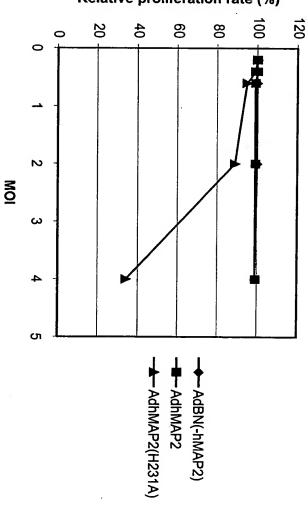


Figure 10

Dominant Negative Variants fo Mehtionine Aminopeptidase Chang et al. 09/943,123 66153/45004

Inventor(s): Appln. No. Docket #

